REVIEWER INDEX

to Volume 124, January–April, 1990

Below is a list of the people who reviewed manuscripts for GENETICS during the preparation of Volume 124. The aim of GENETICS is to communicate significant research. To succeed, we must recognize what is significant, making sure the presentation is accurate, unambiguous and easily readable. For this, we depend heavily on our reviewers, who perform this indispensable service without reward. The quality of the journal strongly reflects the quality of their efforts. We apologize to any reviewer whose name has been inadvertently omitted, and we are sincerely grateful to all.

Aldrich, R.
Ambros, V.
Arnold, J.
Aronow, B.
Avise, J. C.

Barbujani, G.
Bargmann, C.
Barton, N.
Beavis, W. D.
Beckendorf, S. K.
Bender, W.
Björk, G.
Bonierbale, M.
Bostian, K.
Breedon, L.
Brooks, L. D.
Brown, W.
Bürger, R.
Burke, D.

Cartwright, I. L.
Cavener, D.
Charlesworth, B.
Cherbas, L.
Choo, T.-M.
Christiansen, F. D.
Copeland, N.
Costantino, R.
Cox, B.
Cox, E. C.
Coyne, J. A.
Crozier, R. H.
Culbertson, M.

Davis, R. H.
Desalle, R.
Dickinson, W. J.
Doane, W.
Dodds, K. G.
Duncan, I. W.

Eanes, W. F.
Eckardt, F.
Engels, W. R.
Esposito, M. S.
Ewens, W. J.

Folkerts, O.
Frank, S.
Fristrom, J.
Futcher, B.
Fyrberg, E.

Ganal, M.
Ganetzky, B.
Garen, A.
Garland-Campbell, K.
Gillespie, J. H.
Gillham, N. W.
Gimmelfarb, A.
Golding, G. B.
Greenspan, R.
Greenwald, I.
Griffing, B.

Harrison, D.
Hartwell, L. H.
Hastings, A.
Hawley, R. S.
Hedgecock, E. M.
Hedrick, P. W.
Henikoff, S.
Hilliker, A. J.
Hinnebusch, A.
Hodgetts, R. B.
Hoffman, A. A.
Hoffman, R. J.
Hollingsworth, N.
Horabin, J.
Hoyt, M. A.
Husband, B.

Jinks-Robertson, S.
Johnson, T.
Johnston, M.
Johnston, S.
Jones, R. S.

Kalter, H.
Karam, J. D.
Kennedy, B. W.
Kidwell, M. G.
Kingsolver, J.
Klar, A. J. S.
Klein, H.
Knapp, S. J.
Korfhagen, T.
Koshland, D.
Kozak, C.
Kucherlapati, R.
Kunkel, T. A.

Lapis, P.
Last, R.
Lee, M.
Lenski, R.
Lichten, M.
Lim, J. K.
Lipshitz, H.
Livingston, D.
Lloyd, S.
Lynch, M.

Maroni, G.
Mason, J. M.
Matsumoto, K.
McClintock, B.
Melchinger, A.
Messeguer, R.
Meyer, B.
Meyer, H.
Meyerowitz, E.
Miller, B.
Miyamoto, M. M.
Moens, P. B.
Mohler, J. D.
Moody, M.
Moran, C.
Moses, M.
Muskavitch, M. A. T.

Nadeau, J.
Nagylaki, T.
Neuffer, M. G.

Ohta, T.
Orr, A.

Paquin, C.
Pease, C.
Peifer, M.
Penny, D.
Pereira, A.
Petes, T.
Pirrotta, V.
Porter, A.
Pringle, J.

Quiros, C.

Rabinow, L.
Rand, D.
Reynolds, R.
Ripley, L.
Rizki, T. M.
Robertson, H.
Rockmill, B.
Rose, M. D.
Rosenberg, S.
Rothstein, R.
Rouhani, S.
Runge, K.
Russell, P.
Russell, P. J.

Samuels, M.
Schild, D.
Schmid, M.
Schmidt, R. J.
Scott, W.
Sears, E. R.
Second, G.
Sharp, P. M.
Shaw, R.
Shepherd, N.
Simmons, G. M.
Skinner, S.
Slatkin, M.
Smith, G. R.
Smith, P. D.
Snyder, M.
Sofer, W.
Sokal, R. R.
Soller, M.
Sprague, G.
Stahl, F. W.
Stern, D.
Strathern, J.
Stringer, J.

Stuber, C. W.
Szostak, J. W.

Taylor, J. W.
Thaler, D. S.
Tompkins, L.
Tracey, M. L.

Vallejos, E.
Vawter, L.
Vodkin, L.
Voelker, R. A.

Wagner, G. P.
Walsh, J. B.
Wang, Z.
Warner, J. R.
Wasserman, M.
Weber, K. E.
Welker, D. L.
Welshons, W.
Whiteway, M.
Whittam, T. S.
Wigler, M.
Wilhite, F. M.
Winston, F.
Witten, M.
Woodruff, R. C.
Wright, T. R. F.

Yoo, B.
Young, E. T.

Zamir, D.
Zeng, Z.-B.
Zhu, J.
Zouras, E.

AUTHOR INDEX

to Volume 124, January–April 1990

Abel, K. J., 937
Adler, P. N., 145
All-Robyn, J. A., 505
Anderson, W. W., 999
Ashburner, M., 909
Avise, J. C., 397

Baillie, D. L., 615
Barthelmess, I. B., 599
Barton, N., 921
Barton, N. H., 773
Basten, C. J., 187
Beckenbach, A. T., 157
Belmont, L., 523
Bennett, G. D., 949
Bergelson, J., 407, 417
Bhatia, K., 717
Birchler, J. A., 677
Bojko, M., 593
Borts, R. H., 573
Botstein, D., 67, 251
Brettell, R. I. S., 423
Brower, D. L., 899
Brown, J. R., 157
Brown, N., 505
Brunk, B. P., 145
Bullard, D. C., 957
Bulmer, M., 979
Buroker, N. E., 157
Byrd, C. A., 899

Cahaner, A., 783
Carlson, J., 293
Carruthers, D. R., 81
Castilho-Valavicius, B., 483
Cavener, D. R., 873
Chovnick, A., 317, 339
Coffin, J. M., 221
Conley, K., 27
Connelly, C., 237
Corbin, V., 637, 881
Cox-Foster, D. L., 873
Crow, J. F., 207

Daniels, S. B., 339
Denis, C. L., 283
DeVerna, J. W., 735
Diehl, W. J., 687
Donahue, T. F., 483
Doughty, G., 317
Duttaroy, A., 317

Eeley, H., 921
Eggleston, W. B., 331
Engels, W. R., 331
Epperson, B. K., 757

Fabian, G. R., 497
Faugeron, G., 585
Fauron, C. M.-R., 423
Finnell, R. H., 949
Fisher, R. A., 207
Fogel, S., 573
Fotheringham, S., 833
Fox, M. S., 67
Frankel, W. N., 221
Franz, K., 57
Freund, C., 27
Fujimura, H.-A., 275

Gaffney, P. M., 687
Gallais, A., 199
Ganetzky, B., 133
Geer, B. W., 881
Gerring, S. L., 237
Gilbert, T. A., 157
Gillespie, J. H., 447
Gimelfarb, A., 443
Gordon, D. M., 175
Green, M. M., 793
Griffin, E., 505
Gross, K. W., 937

Haber, J. E., 533, 547, 573
Haberfeld, A., 783
Hale, L. R., 995
Hall, B. G., 455, 473
Havlik, M., 423
Heinstra, P. W. H., 881
Herschel, R., 7
Hess, S. M., 497
Hiebert, J. C., 677
Hieter, P., 237
Hilger, F., 797
Hillel, J., 783
Hoffman, C. S., 807
Holloman, W. K., 833
Hopper, A. K., 497
Horowitz, N. H., 1
Hoyt, M. A., 251
Hutter, P., 909
Hyman, B. C., 845

Jeffreys, A. J., 783
Johnsen, R. C., 615
Johnston, G. C., 81
Jones, E. W., 27, 39
Jorde, L. B., 717

Kapoun, A. M., 881
Karwan, A., 57
Keil, R. L., 263
Kelley-Geraghty, D., 505
Kidwell, M. G., 339
Kirkpatrick, M., 979
Kleckner, N., 449
Koehn, R. K., 687
Kramer, B., 573
Kramer, W., 573
Kreber, R., 133
Kruger, D., 599
Kunes, S., 67

Lai, C., 627
Lamas M., G., 921
Lande, R., 743
Lanini, B., 735
Lavi, U., 783
Lemmon, S. K., 27
Leung, W.-Y., 573
Levin, B. R., 175
Liebman, S. W., 505
Lilly, M., 293
Little, J. W., 899
Livak, K. J., 303
Lofsvold, D., 979
Louis, E. J., 533, 547

Mackay, T. F. C., 627
MacRae, A. F., 999
Mallet, J., 921
Malvar, T., 283
Maniatis, T., 637
McCarron, M., 317
McKechnie, S. W., 881
McKim, K. S., 115
McLarnon, C. F., 647, 663
Meyer, B. J., 91
Miller, L. M., 663
Mirfakhrai, M., 607
Mitchell-Olds, T., 407, 417
Moehle, C. M., 39
Mohl, V. K., 949
Moody, M. E., 187
Muedas M., M., 921
Murray, L. E., 81
Murtha, M. T., 873

Nash, D., 889

Nei, M., 967

O'Hara, P. J., 157
Orzack, S. H., 373, 385
Otto, S. P., 429
Ovenden, J. R., 701

Paigen, K., 677
Paluh, J. L., 599
Parker, E. D., Jr., 373
Parker, L. L., 455, 473
Paterson, A. H., 735
Perkins, D. D., 599
Peterson, K. R., 339
Petitjean, A., 797
Plamann, M., 599
Plotzky, Y., 783
Prakash, L., 817
Prakash, S., 817
Prendergast, J. A., 81

Rasmusson, K. E., 647, 663
Raymond, J. D., 647, 663
Reeb, C. A., 397
Reha-Krantz, L. J., 213
Rhounim, L., 585
Roeder, G. S., 561
Roote, J., 909
Rose, A. M., 115
Rosenbluth, R. E., 615
Rossignol, J.-L., 585
Rowley, A., 81
Ruzinski, M. M., 7

Santisteban C., J., 921
Scalfani, R. A., 523
Schaap, T., 783
Schiestl, R. H., 817
Schimenti, J. C., 957
Schonbaum, C. P., 873
Scott, T. M., 687
Sherman, F., 512
Simmons, M. J., 647, 663
Simon, E., 165
Singer, R. A., 81
Singh, R. S., 995
Sitaraman, K., 317
Slater, T. M., 845
Smith, M. J., 157
Smolik-Utlaut, S. M., 357
Spencer, F., 237
Stearns, T., 251
Stern, M., 133
Stevens, L., 367
Stewart, F. M., 175
Stoneking, M., 717
Stoye, J. P., 221
Strausbaugh, L. D., 339
Su, J.-Y., 523
Sved, J. A., 331
Tacthell, K., 797
Takahata, N., 967
Tanaka, Y., 607
Tanksley, S. D., 735
Taylor, B. A., 221
Thomas, J. H., 855
Thomas, W. K., 157
Thompson, R., 743
Tiong, S. Y. K., 889
Turelli, M., 447

Villeneuve, A. M., 91
Voelkel-Meiman, K., 561

Wade, M. J., 367
Wakem, L. P., 512
Walbot, V., 429
White, R. W. G., 701
Williams, S. M., 439
Williamson, M., 573
Wilson, A. C., 717
Winston, F., 807
Wintersberger, U., 57

Yanagisawa, K., 607
Yanofsky, C., 599
Yoon, H., 483
Yuan, L.-W., 263

Zunt, J. R., 663

SUBJECT INDEX

to Volume 124, January–April 1990

Acipenser transmontanus, length heteroplasmy, mitochondrial DNA, 157
Adenosine monophosphate, cyclic, thermosensitive alleles of *CDC25* gene, yeast, 797
Alcohol dehydrogenase
  locus, autosomal dosage compensation, *Drosophila melanogaster*, 677
  molecular control of induction, ethanol, *Drosophila melanogaster*, 881
  nonfermentative and *spt*-mediated gene expression, *CCR4* gene, yeast, 283
Allele
  genealogy, overdominant and frequency-dependent selection, major histocompatibility complex loci, 967
  mutant, *cpc-1*, *Neurospora crassa*, 599
  thermosensitivity, *CDC25* gene in cAMP metabolism, yeast, 797
Allozyme, genetics, incipient speciation, *Galaxias truttaceus*, 701
Aristapedioid, gain of function, homeotic mutation, *Drosophila melanogaster*, 145
Ascobolus immersus, premeiotic gene inactivation, 585
Axon, excitability, Drosophila sodium channel gene, dosage effects, 133

Bacteriophage T4, DNA polymerase, two protein domains, 213
Beadle, George Wells, *in memoriam*, 1
Beetle, flour, cytoplasmically inherited reproductive incompatibility, 367
Behavior
  Drosophila sodium channel gene, axonal excitability, dosage effects, 133
  genetic analysis of defecation, *Caenorhabditis elegans*, 855
  smellblind gene, olfaction in Drosophila, 293
Benomyl, sensitivity to antimicrotubule drugs, yeast mutants, 251
Breeding, gene introgression, DNA fingerprints, 783

Caenorhabditis elegans, 115, 615, 855
Cell cycle
  mutation affecting the division arrest signal, pheromone response pathway, yeast, 275
  size selection, new genes for cell proliferation, yeast, 81
Chromosome
  foundations of genetic fine structure, perspectives, 793
  mitotic intrachromosomal recombination, distance-independence, yeast, 263
  mitotic transmission fidelity mutants, yeast, 237
  overlapping recombinant, mapping of quantitative trait loci, tomato, 735
  second, *adenosine3* region, *Drosophila melanogaster*, 889
Chromosome *I*, duplications on *Caenorhabditis elegans*, 115
Chromosome *X*
  genetic and molecular analysis of *SOE1*, yeast, 523
  hybrid dysgenesis-induced quantitative variation, *Drosophila melanogaster*, 627
Chromosome *Y*, detailed structure of genes and transcripts, *Drosophila melanogaster*, 303
Clathrin, -deficient status, genetic instability, yeast, 27
Crassostrea virginica, genetic discontinuity, mitochondrial DNA, 397
Cytoplasm, inherited reproductive incompatibility, *Tribolium confusum*, 367

Defecation, genetic analysis, *Caenorhabditis elegans*, 855
Deletion, mitochondrial DNA, *Romanomermis culicivorex*, 845
DNA
  conformation, pathways of transformation, *Ustilago maydis*, 833
  damage recovery, pedigree analyses, yeast, 57
  fingerprints, gene introgression, breeding program, 783
  free, synapsis-mediated fusion, inverted dimer plasmids in yeast, 67
  methylation in eukaryotes, mouse, maize, 429
  mismatch repair-induced meiotic recombination, *PMS1* gene product, yeast, 573
  mitochondrial
    genetic discontinuity, *Crassostrea virginica*, 397
    geographic variation, New Guinea, 717
    length heteroplasmy, sturgeon, 157
    mating preferences, *Drosophila pseudoobscura*, 999
    non-neutral selection, variants, 995
    uniparental inheritance, *Polysphondylium palladium*, 607
  mitochondrial deletions, *Romanomermis culicivorex*, 845
  premeiotic gene inactivation, *Ascobolus immersus*, 585
  SRS2 suppressor of *rad6* mutations, yeast, 817
DNA polymerase, two protein domains, bacteriophage T4, 213
Dosage compensation
  autosomal, alcohol dehydrogenase locus, *Drosophila melanogaster*, 677
  sex determination and, *sdc*-1 gene, *Caenorhabditis*

elegans, 91
Drosophila, 133, 293, 339, 909
Drosophila melanogaster, 145, 303, 317, 331, 357, 627, 637, 647, 663, 677, 873, 881, 889, 899
Drosophila pseudoobscura, 995, 999

Environment, -genotype interactions, genetic variation, 443, 447
Escherichia coli, 455, 473
Ethanol, molecular control of induction, alcohol dehydrogenase, *Drosophila melanogaster*, 881
Eukaryotes, DNA methylation, mouse, maize, 429
Evolution
  geographic variation, human mitochondrial DNA, New Guinea, 717
  inheritance and selection, growth trajectories, 979
  mammalian, pattern, relative rate of molecular evolution, 165
  multigene families, natural selection, 439
  second sex ratio, comparative biology, *Nasonia vitripennis*, 385
  subdivided populations, latent genes, 187
  subtelomeric Y^+ repeat family, yeast, 533

Fisher, R.A., perspectives on genetics, 207
Fluctuation analysis, mutants under different conditions, 175

Galaxias truttaceus, mitochondrial and allozyme genetics, incipient speciation, landlocked population, 701
Gene
  adenosine3 region of second chromosome, *Drosophila melanogaster*, 889
  alcohol dehydrogenase, *cis*-regulatory elements, *Drosophila melanogaster*, 637
  CCR4, nonfermentative and *spt*-mediated gene expression, yeast, 283
  CDC25, thermosensitive alleles, cAMP metabolism in yeast, 797
  complementary, inviability of hybrids, *Drosophila* sibling species, 909
  conversion, mechanisms, *Saccharomyces cerevisiae*, 7
  cpc-1, inactivating alterations, mutant alleles of *Neurospora crassa*, 599
  detailed structure and transcripts, *Drosophila melanogaster*, 303
  fbp1 gene expression, *Schizosaccharomyces pombe*, 807
  fine structure, perpectives, 793
  flow and selection, cline width and linkage disequilibrium, heliconius hybrid zones, 921
  homeotic, *abx/bx/pbx* mutations, *Drosophila melanogaster*, 899
  horizontal transmission, *P* transposable element, *Drosophila* species, 339
  interchromosomal conversion, *HOT1*, yeast, 561
  introgression, DNA fingerprints, breeding program, 783
  latent, evolution, subdivided populations, 187
  multigene families, natural selection, 439
  PMS1, mismatch repair-induced meiotic recombination, yeast, 573
  PRB1, expression in yeast, 39
  premeiotic, inactivation, *Ascobolus immersus*, 585
  sdc-1, sex determination and dosage compensation, *Caenorhabditis elegans*, 91
  smellblind, olfaction in Drosophila, 293
  SOE1, genetic and molecular analysis, yeast, 523
Genome, mitochondrial, maize fertile cmsT revertant line, recombination, 423
Genotype
  -environment interactions, genetic variation, 443, 447
  spatial autocorrelation, directional selection, 757
Glucose
  expression of *PRB1* gene, yeast, 39
  fbp1 gene expression, *Schizosaccharomyces pombe*, 807
Glucose dehydrogenase, developmental expression of gene, *Drosophila melanogaster*, 873

Heat shock, lymphocyte response, duration, mouse, 949
Heteroplasmy, length, mitochondrial DNA, sturgeon, 157
Heterozygote, deficiency, *Mulinia lateralis*, 687
Hybrid dysgenesis
  germ-line and somatic recombination, modified *P* elements, *Drosophila melanogaster*, 331
  -induced quantitative variation, *X* chromosome, *Drosophila melanogaster*, 627
  P element-mediated, repression, *Drosophila melanogaster*, 663
  quantitative effects of *P* elements, *Drosophila melanogaster*, 647
Hybrids, inviability between sibling species, *Drosophila*, 909

Impatiens capensis, statistical genetics, 407
Inheritance
  selection and evolution, growth trajectories, 979
  uniparental, mitochondrial DNA polymorphism, *Polysphondylium palladium*, 607
Insertion, genetic rearrangements at renin loci, physical characterization, mouse, 937
Inversion loops, synaptic adjustment, *Neurospora crassa*, 593

Leukemia, proviruses, linkage map, mouse, 221
Linkage disequilibrium, cline width and, selection and gene flow, heliconius hybrid zones, 921
Lycopersicon esculentum, 735
Lymphocytes, heat shock response duration, genetic differences, mouse, 949

Maize
DNA methylation in eukaryotes, 429
fertile cmsT revertant line, mitochondrial genome, 423
Major histocompatibility complex, allelic genealogy, overdominant and frequency-dependent selection, 967
Mapping
chromosome *I* duplications, *Caenorhabditis elegans*, 115
clathrin-deficeint status, genetic instability, yeast, 27
linkage, murine leukemia proviruses, 221
quantitative trait loci, overlapping recombinant chromosomes, tomato, 735
t complex responder candidate gene family, molecular cloning, mouse, 957
Maternal effects, statistical genetics, *Impatiens capensis*, 407
Mating
mitochondrial DNA polymorphism, uniparental inheritance, *Polysphondylium palladium*, 607
mitochondrial DNA variants, non-neutral selection, 995
mutation affecting the division arrest signal, pheromone response pathway, yeast, 275
preferences, changes in mtDNA haplotype frequencies, 999
Meiosis
chromosome *I* duplications, *Caenorhabditis elegans*, 115
foundations of genetic fine structure, perspectives, 793
genetic and molecular analysis of *SOE1*, yeast, 523
mismatch repair-induced recombination, *PMS1* gene product, yeast, 573
pairing for recombination in LGV, *Caenorhabditis elegans*, 615
Mitochondria
allozyme genetics, incipient speciation, *Galaxias truttaceus*, 701
DNA, geographic variation, New Guinea, 717
genetic and molecular analysis of *SOE1*, yeast, 523
Mitosis
chromosome transmission fidelity mutants, yeast, 237
interchromosomal gene conversion, *HOT1*, yeast, 561
intrachromosomal recombination, distance-independence, yeast, 263
recombination, subtelomeric Y′ repeats, yeast, 547
Mouse
DNA methylation in eukaryotes, 429
leukemia proviruses, linkage map, 221
lymphocyte heat shock response, duration, genetic differences, 949
renin loci, physical characterization, genetic rearrangements, 937
t complex responder candidate gene family, molecular cloning, genetic mapping, 957
Mulinia lateralis, interrelationships of heterozygosity, growth rate, heterozygote deficiencies, 687
Mutants
chromosome transmission fidelity, yeast, 237
fluctuation analysis, 175
Neurospora crassa allele, *cpc-1*, inactivating alterations, 599
Schizosaccharomyces pombe, *fbp1* gene expression, 807
size selection, new genes for cell proliferation, yeast, 81
yeast, sensitivity, antimicrotubule drugs, 251
Mutations
abx/bx/pbx, homeotic gene expression, *Drosophila melanogaster*, 899
genetic and molecular analysis of *SOE1*, yeast, 523
homeotic, *Aristapedioid* gain of function, *Drosophila melanogaster*, 145
pleiotropic models of quantitative variation, 773
rad6, *SRS2* suppressor, yeast, 817
recovery from DNA damage, pedigree analyses, yeast, 57
snf, expression of *PRB1* gene, yeast, 39
yeast, division arrest signal, pheromone response pathway, 275

Nasonia vitripennis
comparative biology, second sex ratio evolution, 385
genetic variation for sex ratio traits, natural population, 373
Nematode, mitochondrial DNA deletions, 845
Neurospora crassa
mutant alleles, inactivation alterations, *cpc-1*, 599
synaptic adjustment on inversion loops, 593

Olfaction, *smellblind* gene, 293
Operon
cryptic *cel*
mechanisms of activation, *Escherichia coli*, 473
nucleotide sequence, *Escherichia coli*, 455
Oyster, genetic discontinuity, mitochondrial DNA, 397

P elements
alcohol dehydrogenase gene, *cis*-regulatory elements, *Drosophila melanogaster*, 637
Aristapedioid gain of function, homeotic mutation, *Drosophila melanogaster*, 145
horizontal transmission, *Drosophila* species, 339
male recombination and, *Drosophila melanogaster*, 317
-mediated hybrid dysgenesis, repression, *Drosophila melanogaster*, 663
quantitative effects, hybrid dysgenesis, *Drosophila melanogster*, 647

Pheromone, response pathway, division arrest signal, yeast mutation, 275
Phototaxis, *smellblind* gene, olfaction in Drosophila, 293
Plasmids, inverted dimer, synapsis-mediated fusion of free DNA, yeast, 67
Pleiotropy, models of quantitative variation, 773
Polymorphism
  geographic variation, human mitochondrial DNA, New Guinea, 717
  mapping of quantitative trait loci, overlapping recombinant chromosomes, tomato, 735
  marker-assisted selection, improvement, quantitative traits, 783
  overdominant and frequency-dependent selection, allelic genealogy, 967
  subdivided populations, evolution, latent genes, 187
Polyploidy, clathrin-deficient status, genetic instability, yeast, 27
Polysphondylium palladium, mitochondrial DNA polymorphism, uniparental inheritance, 607
Population
  cytoplasmically inherited reproductive incompatibility, *Tribolium confusum*, 367
  doubled haploid, application to theory, line development, 199
  genetic discontinuity, mitochondrial DNA, *Crassostrea virginica*, 397
  genotype-environment interactions, genetic variation, 443, 447
  mating preferences, changes in mtDNA haplotype, *Drosophila pseudoobscura*, 999
  natural, sex ratio traits, *Nasonia vitripennis*, 373
Protease B, expression of *PRB1* gene, yeast, 39
Proviruses, murine leukemia, linkage map, 221

Recombination
  genetic rearrangements at renin loci, physical characterization, mouse, 937
  germ-line and somatic, modified *P* elements, *Drosophila melanogaster*, 331
  maize fertile cmsT revertant line, mitochondrial genome, 423
  male, *P* elements, *Drosophila melanogaster*, 317
  mismatch repair-induced meiotic, *PMS1* gene product, yeast, 573
  mitotic, subtelomeric Y′ repeats, yeast, 547
  mitotic interchromosomal gene conversion, *HOT1*, yeast, 561
  mitotic intrachromosomal, distance-independence, yeast, 263
  overlapping recombinant chromosomes, mapping of quantitative trait loci, tomato, 735
  pairing in LGV, *Caenorhabditis elegans*, 615
  pathways of transformation, DNA conformation, *Ustilago maydis*, 833
  synapsis-mediated fusion of free DNA, inverted dimer plasmids, yeast, 67
Renin, loci, genetic rearrangements, mouse, 937
Reproduction, cytoplasmically inherited incompatibility, *Tribolium confusum*, 367
Retroviruses, murine leukemia proviruses, linkage map, 221
RNA
  detailed structure of genes and transcripts, *Drosophila melanogaster*, 303
  ribosomal, processing defect suppressor, yeast, 497
Romanomermis culicivorex, mitochondrial DNA deletions, 845

Saccharomyces cerevisiae, 7, 27, 39, 57, 67, 81, 237, 251, 263, 275, 293, 483, 497, 505, 512, 523, 533, 547, 561, 573, 797, 817
Schizosaccharomyces pombe, *fbp1* gene expression, mutants, 807
Selection
  directional, spatial autocorrelation, genotypes, 757
  doubled haploid populations, application to theory, line development, 199
  gene flow and, cline width and linkage disequilibrium, heliconius hybrid zones, 921
  inheritance and evolution, growth trajectories, 979
  marker-assisted, improvement, quantitative traits, 743
  natural, multigene families, 439
  non-neutral, mitochondrial DNA variants, 995
  overdominant and frequency-dependent, allelic genealogy, major histocompatibility complex loci, 967
  pleiotropic models of quantitative variation, 773
  statistical genetics, *Impatiens capensis*, 407
Sex determination, gene dosage and, *sdc-1* gene, *Caenorhabditis elegans*, 91
Sex ratio
  second, evolution, *Nasonia vitripennis*, 385
  traits within a natural population, genetic variation, *Nasonia vitripennis*, 373
Sexual differentiation, developmental expression, glucose dehydrogenase gene, *Drosophila melanogaster*, 873
Sodium channel, dosage effects on gene, behavior and axonal excitability, *Drosophila*, 133
Speciation
  incipient, mitochondrial and allozyme genetics, *Galaxias truttaceus*, 701
  inviability of hybrids, sibling species, *Drosophila*, 909
Spermatogenesis, detailed structure of genes and transcripts, *Drosophila melanogaster*, 303
Strains, duration of lymphocyte heat shock response, mouse, 949
Sturgeon, length heteroplasmy, mitochondrial DNA, 157
Sugar
  mechanisms of activation, cryptic *cel* operon, *Escherichia coli*, 473

nucleotide sequence of cryptic *cel* operon, *Escherichia coli*, 455
Suppressors
omnipotent, isolation, yeast, 505, 512
srd1, pre-rRNA processing defect, yeast, 497
SRS2, *rad6* mutations, yeast, 817
translational initiation, *HIS4* expression, yeast, 483
Synapsis, -mediated fusion of free DNA, inverted dimer plasmids, yeast, 67
Synaptonemal complex, synaptic adjustment of inversion loops, *Neurospora crassa*, 593

Telomere
subtelomeric Y^+ repeat family, yeast, 533
subtelomeric Y′ repeats, mitotic recombination, yeast, 547
Temperature
-sensitive pre-rRNA processing defect of *rrp1-1*, *srd1* suppressor, yeast, 497
thermosensitive alleles of *CDC25* gene, cAMP metabolism, yeast, 797
t haplotype, *t complex responder* candidate gene family, molecular cloning and mapping, mouse, 957
Thymidylate kinase, genetic and molecular analysis of *SOE1*, yeast, 523
Tomato, mapping of quantitative trait loci, overlapping recombinant chromosomes, 735
Transcription, alcohol dehydrogenase gene, *cis*-regulatory elements, *Drosophila melanogaster*, 637
Transformation
pathway, DNA conformation, *Ustilago maydis*, 833
synapsis-mediated fusion of free DNA, inverted dimer plasmids, yeast, 67
Translation
initiation suppressors, *HIS4* expression, yeast, 483
isolation of omnipotent suppressors, yeast, 505, 512
Transposable elements
germ-line and somatic recombination, modified *P* elements, *Drosophila melanogaster*, 331
horizontal transmission, *P* transposable element, *Drosophila* species, 339
perspectives, 449
Transposon, quantitative effects of *P* elements, hybrid dysgenesis, *Drosophila melanogaster*, 647
Tribolium confusum, cytoplasmically inherited reproductive incompatibility, 367

Ultrabithorax, *bithoraxoid* and, dosage requirements, *Drosophila melanogaster*, 357
Ustilago maydis, pathways of transformation, DNA conformation, 833

Wasp
comparative biology, second sex ratio evolution, 385
genetic variation for sex ratio traits, natural population, 373

Yeast
cell proliferation, size selection, new genes, 81
chromosome containing *HOT1* preferentially, mitotic interchromsomal gene conversion, 561
clathrin-deficient status, genetic instability, 27
distance-independence, mitotic intrachromosomal recombination, 263
expression of *PRB1* gene, 39
genetic and molecular analysis of *SOE1*, 523
inverted dimer plasmids, synapsis-mediated fusion, free DNA, 67
isolation of omnipotent suppressors, 505, 512
mechanisms of gene conversion, 7
mismatch repair-induced meiotic recombination, *PMS1* gene product, 573
mitotic chromosome transmission fidelity mutants, 237
mutants, sensitivity, antimicrotubule drugs, 251
mutation affecting the division arrest signal, pheromone response pathway, 275
nonfermentative and *spt*-mediated gene expression, *CCR4* gene, 283
pedigree analyses, recovery from DNA damage, 57
srd1 suppressor, temperature-sensitive pre-rRNA processing defect, *rrp1-1*, 497
SRS2 suppressor of *rad6* mutations, 817
subtelomeric Y′ repeat family, 533
subtelomeric Y^+ repeats, mitotic recombination, 547
thermosensitive alleles of *CDC25* gene, cAMP metabolism, 797
translational initiation suppressors, *HIS4* expression, 483

TABLE OF CONTENTS

to Volume 124, January–April, 1990

ABEL, KENNETH J., and KENNETH W. GROSS, Physical characterization of genetic rearrangements at the mouse renin loci 937–947

ALL-ROBYN, JAMIE A., DOROTHY KELLEY-GERAGHTY, EDWARD GRIFFIN, NINA BROWN and SUSAN W. LIEBMAN, Isolation of omnipotent suppressors in an [*eta*$^+$] yeast strain 505–514

BARTON, N. H., Pleiotropic models of quantitative variation 773–782

BIRCHLER, JAMES A., JOHN C. HIEBERT and KENNETH PAIGEN, Analysis of autosomal dosage compensation involving the alcohol dehydrogenase locus in *Drosophila melanogaster* 677–686

BOJKO, MAJA, Synaptic adjustment of inversion loops in *Neurospora crassa* 593–598

BORTS, RHONA H., WAI-YING LEUNG, WILFRIED KRAMER, BARBARA KRAMER, MARSHA WILLIAMSON, SEYMOUR FOGEL and JAMES E. HABER, Mismatch repair-induced meiotic recombination requires the *PMS1* gene product 573–584

BRUNK, BRIAN P., and PAUL N. ADLER, *Aristapedioid*: a gain of function, homeotic mutation in *Drosophila melanogaster* 145–156

BULLARD, DANIEL C., and JOHN C. SCHIMENTI, Molecular cloning and genetic mapping of the *t complex responder* candidate gene family 957–966

BUROKER, N. E., J. R. BROWN, T. A. GILBERT, P. J. O'HARA, A. T. BECKENBACH, W. K. THOMAS and M. J. SMITH, Length heteroplasmy of sturgeon mitochondrial DNA; an illegitimate elongation model 157–163

CASTILHO-VALAVICIUS, BEATRIZ, HEEJEONG YOON and THOMAS F. DONAHUE, Genetic characterization of the *Saccharomyces cerevisiae* translation initiation suppressors *sui1*, *sui2* and *SUI3* of their effects on *HIS4* expression 483–495

CORBIN, VICTORIA, and TOM MANIATIS, Identification of *cis*-regulatory elements required for larval expression of the *Drosophila melanogaster* alcohol dehydrogenase gene 637–646

COX-FOSTER, DIANA L., CHRISTOPHER P. SCHONBAUM, MICHAEL T. MURTHA and DOUGLAS R. CAVENER, Developmental expression of the glucose dehydrogenase gene in *Drosophila melanogaster* 873–880

CROW, JAMES R., R. A. FISHER, A centennial view 207–211

DANIELS, STEPHEN B., KENNETH R. PETERSON, LINDA D. STRAUSBAUGH, MARGARET G. KIDWELL and ARTHUR CHOVNICK, Evidence for horizontal transmission of the *P* transposable element between *Drosophila* species 339–355

DENIS, CLYDE L., and THOMAS MALVAR, The *CCR4* gene from *Saccharomyces cerevisiae* is required for both nonfermentative and *spt*-mediated gene expression 283–291

DUTTAROY, ATANU, MARGARET MCCARRON, KALAVATHY SITARAMAN, GLENN DOUGHTY and ARTHUR CHOVNICK, The relationship between *P* elements and male recombination in *Drosophila melanogaster* 317–329

EASTEAL, SIMON, The pattern of mammalian evolution and the relative rate of molecular evolution 165–173

EPPERSON, B. K., Spatial autocorrelation of genotypes under directional selection 757–771

FABIAN, GARY R., SUZANNE M. HESS and ANITA K. HOPPER, *srd1*, a *Saccharomyces cerevisiae* suppressor of the temperature-sensitive pre-rRNA processing defect of *rrp1-1* 497–504

FAUGERON, GODELEINE, LAÏLA RHOUNIM and JEAN-LUC ROSSIGNOL, How does the cell count the number of ectopic copies of a gene in the premeiotic inactivation process acting in *Ascobolus immersus*? 585–591

FAURON, C. M.-R., M. HAVLIK and R. I. S. BRETTELL, The mitochondrial genome organization of a maize fertile cmsT revertant line is generated through recombination between two sets of repeats 423–428

FOTHERINGHAM, SCOTT, and WILLIAM K. HOLLOMAN, Pathways of transformation in *Ustilago maydis* determined by DNA conformation 833–843

FRANKEL, WAYNE N., JOHNATHAN P. STOYE, BENJAMIN A. TAYLOR and JOHN M. COFFIN, A linkage map of endogenous murine leukemia proviruses 221–236

FUJIMURA, HIRO-AKI, Identification and characterization of a mutation affecting the division arrest signaling of the pheromone response pathway in *Saccharomyces cerevisiae* .. 275–282

GAFFNEY, PATRICK M., TIMOTHY M. SCOTT, RICHARD K. KOEHN and WALTER J. DIEHL, Interrelationships of heterozygosity, growth rate and heterozygote deficiencies in the coot clam, *Mulinia lateralis* 687–699

GALLAIS, A., Quantitative genetics of doubled haploid populations and application to the theory of line development 199–206

GILLESPIE, JOHN H., and MICHAEL TURELLI, Genotype-environment interactions: a reply 447

GIMELFARB, A., How much variation can be maintained by genotype-environment interactions? 443–445

GREEN, M. M., The foundations of genetic fine structure: a retrospective from memory 793–796

HILLEL, J., T. SCHAAP, A. HABERFELD, A. J. JEFFREYS, Y. PLOTZKY, A. CAHANER and U. LAVI, DNA fingerprints applied to gene introgression in breeding programs 783–789

HOFFMAN, CHARLES S., and FRED WINSTON, Isolation and characterization of mutants constitutive for expression of the *fbp1* gene of *Schizosaccharomyces pombe* 807–816

HOROWITZ, NORMAN H., GEORGE WELLS BEADLE (1903–1989) 1–6

HUTTER, PIERRE, JOHN ROOTE and MICHAEL ASHBURNER, A genetic basis for the inviability of hybrids between sibling species of *Drosophila* 909–920

HYMAN, BRADLEY C., and TED M. SLATER, Recent appearance and molecular characterization of mitochondrial DNA deletions within a defined nematode pedigree 845–853

KAPOUN, ANN M., BILLY W. GEER, PIETER W. H. HEINSTRA, VICTORIA CORBIN and STEPHEN W. MCKECHNIE, Molecular control of the induction of alcohol dehydrogenase by ethanol in *Drosophila melanogaster* larvae 881–888

KIRKPATRICK, MARK, DAVID LOFSVOLD and MICHAEL BULMER, Analyisis of the inheritance, selection and evolution of growth trajectories 979–993

KLECKNER, NANCY, Regulating Tn*10* and IS*10* transposition 449–454

KLEIN, FRANZ, ANNELIESE KARWAN and ULRIKE WINTERSBERGER, Pedigree analyses of yeast cells recovering from DNA damage allow assignment of lethal events to individual post-traumatic generations 57–65

KUNES, SAM, DAVID BOTSTEIN and MAURICE S. FOX, Synapsis-mediated fusion of free DNA ends forms inverted dimer plasmids in yeast 67–80

LAI, CHAOQIANG, and TRUDY F. C. MACKAY, Hybrid dysgenesis-induced quantitative variation on the *X* chromosome of *Drosophila melanogaster* 627–636

LANDE, RUSSELL, and ROBIN THOMPSON, Efficiency of marker-assisted selection in the improvement of quantitative traits 743–756

LEMMON, SANDRA K., CAROL FREUND, KATHLEEN CONLEY and ELIZABETH W. JONES, Genetic instability of clathrin-deficient strains of *Saccharomyces cerevisiae* 27–38

LILLY, MARY, and JOHN CARLSON, *smellblind*: a gene required for Drosophila olfaction 293–302

LITTLE, JOHN W., CHRISTINE A. BYRD and DANNY L. BROWER, Effect of *abx*, *bx* and *pbx* mutations on expression of homeotic genes in Drosophila larvae 899–908

LIVAK, KENNETH J., Detailed structure of the *Drosophila melanogaster Stellate* genes and their transcripts 303–316

LOUIS, EDWARD J., and JAMES E. HABER, The subtelomeric Y′ repeat family in *Saccharomyces cerevisiae*: an experimental system for repeated sequence evolution 533–545

LOUIS, EDWARD J., and JAMES E. HABER, Mitotic recombination among subtelomeric Y′ repeats in *Saccharomyces cerevisiae* 547–559

MacRae, Amy F., and Wyatt W. Anderson, Can mating preferences explain changes in mtDNA haplotype frequencies? 999–1001

Mallet, James, Nick Barton, Gerardo Lamas M., José Santisteban C., Manuel Muedas M. and Harriet Eeley, Estimates of selection and gene flow from measures of cline width and linkage disequilibrium in Heliconius hybrid zones 921–936

McKim, Kim S., and Ann M. Rose, Chromosome *I* duplications in *Caenorhabditis elegans* 115–132

Mirfakhrai, Miranda, Yoshimasa Tanaka and Kaichiro Yanagisawa, Evidence for mitochondrial DNA polymorphism and uniparental inheritance in the cellular slime mold *Polysphondylium pallidum*: effect of intraspecies mating on mitochondrial DNA transmission 607–613

Mitchell-Olds, Thomas, and Joy Bergelson, Statistical genetics of an annual plant, *Impatiens capensis*. II. Natural selection 417–421

Moehle, Charles M., and Elizabeth W. Jones, Consequences of growth media, gene copy number, and regulatory mutations on the expression of the *PRB1* gene of *Saccharomyces cerevisiae* 39–55

Moody, Michael E., and Christopher J. Basten, The evolution of latent genes in subdivided populations 187–197

Mohl, Virginia K., Gregory D. Bennett and Richard H. Finnell, Genetic differences in the duration of the lymphocyte heat shock response in mice 949–955

Orzack, Steven Hecht, The comparative biology of second sex ratio evolution within a natural population of a parasitic wasp, *Nasonia vitripennis* 385–396

Orzack, Steven Hecht, and E. Davis Parker, Jr., Genetic variation for sex ratio traits within a natural population of a parasitic wasp, *Nasonia vitripennis* 373–384

Otto, Sarah P., and Virginia Walbot, DNA methylation in eukaryotes: kinetics of demethylation and *de novo* methylation during the life cycle 429–437

Ovenden, J. R., and R. W. G. White, Mitochondrial and allozyme genetics of incipient speciation in a landlocked population of *Galaxias truttaceus* (Pisces: Galaxiidae)..... 701–716

Paluh, Janet L., Michael Plamann, Dirk Krüger, Ilse B. Barthelmess, Charles Yanofsky and David D. Perkins, Determination of the inactivating alterations in two mutant alleles of the *Neurospora crassa* cross-pathway control gene *cpc-1* 599–606

Parker, Laura L., and Barry G. Hall, Characterization and nucleotide sequence of the cryptic *cel* operon of *Escherichia coli* K12 455–471

Parker, Laura L., and Barry G. Hall, Mechanisms of activation of the cryptic *cel* operon of *Escherichia coli* K12 473–482

Paterson, Andrew H., Joseph W. DeVerna, Brenda Lanini and Steven D. Tanksley, Fine mapping of quantitative trait loci using selected overlapping recombinant chromosomes, in an interspecies cross of tomato 735–742

Petitjean, Anne, François Hilger and Kelly Tatchell, Comparison of thermosensitive alleles of the *CDC25* gene involved in the cAMP metabolism of *Saccharomyces cerevisiae* 797–806

Prendergast, J. A., L. E. Murray, A. Rowley, D. R. Carruthers, R. A. Singer and G. C. Johnston, Size selection identifies new genes that regulate *Saccharomyces cerevisiae* cell proliferation 81–90

Rasmusson, Korise E., Michael J. Simmons, John D. Raymond and Christopher F. McLarnon, Quantitative effects of *P* elements on hybrid dysgenesis in *Drosophila melanogaster* 647–662

Reeb, Carol A., and John C. Avise, A genetic discontinuity in a continuously distributed species: mitochondrial DNA in the American oyster, *Crassostrea virginica* 397–406

Reha-Krantz, Linda J., Genetic evidence for two protein domains and a potential new activity in bacteriophage T4 DNA polymerase 213–220

Roman, Herschel, and Mary M. Ruzinski, Mechanisms of gene conversion in *Saccharomyces cerevisiae* 7–25

ROSENBLUTH, RAJA E., ROBERT C. JOHNSEN and DAVID L. BAILLIE, Pairing for recombination in LGV of *Caenorhabditis elegans*: a model based on recombination in deficiency heterozygotes 615–625

SCHIESTL, ROBERT H., SATYA PRAKASH and LOUISE PRAKASH, The *SRS2* suppressor of *rad6* mutations of *Saccharomyces cerevisiae* acts by channeling DNA lesions into the *RAD52* DNA repair pathway 817–831

SIMMONS, MICHAEL J., JOHN D. RAYMOND, KORISE E. RASMUSSON, LOREN M. MILLER, CHRISTOPHER F. MCLARNON and JOSEPH R. ZUNT, Repression of *P* element-mediated hybrid dysgenesis in *Drosophila melanogaster* 663–676

SINGH, RAMA S., and LARRY R. HALE, Are mitochondrial DNA variants selectively neutral? 995–997

SMOLIK-UTLAUT, SARAH M., Dosage requirements of *Ultrabithorax* and *bithoraxoid* in the determination of segment identity in *Drosophila melanogaster* 357–366

SPENCER, F., S. L. GERRING, C. CONNELLY and P. HIETER, Mitotic chromosome transmission fidelity mutants in *Saccharomyces cerevisiae* 237–249

STEARNS, TIM M., ANDREW HOYT and DAVID BOTSTEIN, Yeast mutants sensitive to antimicrotubule drugs define three genes that affect microtubule function 251–262

STERN, MICHAEL, ROBERT KREBER and BARRY GANETZKY, Dosage effects of a Drosophila sodium channel gene on behavior and axonal excitability 133–143

STEVENS, LORI, and MICHAEL J. WADE, Cytoplasmically inherited reproductive incompatibility in Tribolium flour beetles: the rate of spread and effect on population size 367–372

STEWART, FRANK M., DAVID M. GORDON and BRUCE R. LEVIN, Fluctuation analysis: the probability distribution of the number of mutants under different conditions 175–185

STONEKING, MARK, LYNN B. JORDE, KULDEEP BHATIA and ALLAN C. WILSON, Geographic variation in human mitochondrial DNA from Papua New Guinea 717–733

SU, JIN-YUAN, LISA BELMONT and ROBERT A. SCLAFANI, Genetic and molecular analysis of the *SOE1* gene: a $tRNA_3^{Glu}$ missense suppressor of yeast *cdc8* mutations 523–531

SVED, JOHN A., WILLIAM B. EGGLESTON and WILLIAM R. ENGELS, Germ-line and somatic recombination induced by *in vitro* modified *P* elements in *Drosophila melanogaster* 331–337

TAKAHATA, NAOYUKI, and MASATOSHI NEI, Allelic genealogy under overdominant and frequency-dependent selection and polymorphism of major histocompatibility complex loci 967–978

THOMAS, JAMES H., Genetic analysis of defecation in *Caenorhabditis elegans* 855–871

TIONG, S. Y. K., and DAVID NASH, Genetic analysis of the *adenosine3* (*Gart*) region of the second chromosome of *Drosophila melanogaster* 889–897

VILLENEUVE, ANNE M., and BARBARA J. MEYER, The role of *sdc-1* in the sex determination and dosage compensation decisions in *Caenorhabditis elegans* 91–114

VOELKEL-MEIMAN, KAREN, and G. SHIRLEEN ROEDER, A chromosome containing *HOT1* preferentially receives information during mitotic interchromosomal gene conversion 561–572

WAKEM, L. PAUL, and FRED SHERMAN, Isolation and characterization of omnipotent suppressors in the yeast *Saccharomyces cerevisiae* 512–522

WILLIAMS, SCOTT M., The opportunity for natural selection on multigene families 439–441

YUAN, LING-WEN, and RALPH L. KEIL, Distance-independence of mitotic intrachromosomal recombination in *Saccharomyces cerevisiae* 263–273